

## Clinical and Research Genomics Assignment #3

From Lecture\_07-09 (April 4<sup>th</sup>):

### RNA-Sequencing, Epigenomes, DNA Modifications, and Chromatin Dynamics

---

**Assignment: Answer questions about epigenomics and DNA modifications**

**Due Date: 5:00PM on April 21<sup>st</sup>**

---

#### Epigenome and DNA Modifications

Analyze and Contextualize DNA Methylation data from a RRBS experiment

If you do not already have it installed, install the free statistical program R on your computer:

<http://www.r-project.org/>

You can use the slides on this blog to understand the algorithms that we have discussed in class:

<http://zvfak.blogspot.com/2013/03/epiworkshop-2013-dna-methylation.html>

If you have trouble getting the package for R from the tutorial, you can download it here:

<http://code.google.com/p/methylkit/>

---

Utilize the tutorial to familiarize yourself with R and the program.

Then, from the test dataset within the package, your assignment is to:

1. Check if there is an indication of PCR bias in the experiment.
  2. Calculate # of differentially methylated cytosines (DMCs)
  3. Annotate the DMCs with genes and discuss implications of that annotation.
  4. Check correlation between samples.
  5. Cluster samples to see if replicates cluster together
- 

**Please hand the assignment on the day of the lecture, or email if you cannot attend.**

**For any questions, please contact Chandrima Bhattacharya ([chb4004@med.cornell.edu](mailto:chb4004@med.cornell.edu)), Ebrahim Afshinnekoo ([eba2001@med.cornell.edu](mailto:eba2001@med.cornell.edu)), or Professor Mason ([chm2042@med.cornell.edu](mailto:chm2042@med.cornell.edu))**